

学 位 論 文 要 旨	
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題 目	Identification of mycorrhizal communities and fungal specificities in three epiphytic orchid species. (ラン科着生 3 種における菌根菌相の特定と菌特異性の比較検証)
<p>Orchidaceae is one of the largest plant families, containing approximately 28,000 species, which are highly diversified in their habits and include terrestrial, epiphytic and lithophytic species. In particular, epiphytic orchids are the most diversified form, accounting for 69% of all orchid species and 68% of all vascular epiphytes. All orchids have dust-like seeds containing few stored nutrients and thus depend entirely on mycorrhizal fungi for carbon supply during seed germination and subsequent establishment of seedlings. This association generally persists in adult plants. Mycorrhizal associations may be more important for epiphytic orchids than terrestrial species, as they may aid survival in the canopy under strong environmental stresses such as low water and nutrient availabilities. However, few studies have examined the mycorrhizal association of epiphytic orchids. Here, we investigated the mycorrhizal community of three epiphytic orchid species, using more samples than in any previous study. We assessed the mycorrhizal communities of <i>Taeniophyllum glandulosum</i> and <i>Thrixspermum japonicum</i>, which are the most common epiphytic orchids in the temperate region of Japan, and <i>Dendrobium okinawense</i> that is an endangered epiphytic orchid in sub-tropical region of Japan. In total, we collected 187 samples from 80 individuals at 14 sites for <i>T. glandulosum</i>, 191 samples from 144 individuals at 20 sites for <i>T. japonicum</i> and 25 samples from 10 individuals at four sites for <i>D. okinawense</i>. The mycorrhizal fungi were identified based on nuclear ribosomal DNA internal transcribed spacer sequences and assigned operational taxonomic units (OTUs) based on 97% sequence similarity. Obtained mycorrhizal communities are clearly different depending on orchid species. <i>T. glandulosum</i> was specifically associated with a single Ceratobasidiaceae OTU, which detected from 90% of all samples. <i>D. okinawense</i> was specifically associated with a single Tulasnellaceae OTU: this fungus was identified from all samples. In contrast to these species, <i>T. japonicum</i> are associated with a broad range of fungi belonged to the Ceratobasidiaceae and Tulasnellaceae. However, a single Ceratobasidiaceae OTU accounted for 50% of all fungal sequences and was predominant in samples from 15 host tree species and 12 sites. Our results suggest that mycorrhizal communities of epiphytic orchid species are quite different among species and fungal specificities are varied from highly specific association with almost a single fungal species to broad interaction with multiple fungal species. This study contributes to elucidating mycorrhizal symbiosis in epiphytic orchids. Furthermore, our findings also contribute to establishing the <i>in vitro</i> mass-propagation of endangered orchids and also epiphytic species for horticultural uses by using mycorrhizal fungi.</p>	